

## SEQUENCE LISTING

<110> Fox, Brian  
Holloway, James L.

<120> ADIPOCYTE COMPLMENT RELATED PROTEIN  
ZACRP13

<130> 00-96

<150> US 60/253,924  
<151> 2000-11-29

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<222> (2)...(1381)

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gtt gct gga cct cca gca cac ccc agg ccc cca gaa gaa gtc ggg cct 97  
Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro  
20 25 30

~~cct ggt gca cca ggt tta cca caa tat aca gga gaa ata agt gaa atg~~ 145  
~~Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met~~  
33 35 40 45

~~aca aaa tgc ccc tgt cct gat ata gaa agg tca~~ ~~gcc~~ ttt act gtg aag 193  
Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys  
50 55 60

ctc	agt	gga	aaa	ctt	cct	ctt	cct	ttc	aag	ccc	atc	atc	ttc	aca	ggg	241
Leu	Ser	Gly	Lys	Leu	Pro	Leu	Pro	Phe	Lys	Pro	Ile	Ile	Phe	Thr	Gly	
65				70					75				80			
gtc	ctg	tac	aat	gcc	cag	agg	gat	tta	aag	gag	gcc	atg	gga	gtc	ttt	289
Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys	Glu	Ala	Met	Gly	Val	Phe	
				85					90				95			
gct	tgc	agg	gtg	cct	ggg	aat	tac	tac	tcc	agc	ttt	gat	gtt	gag	ctg	337
Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser	Ser	Phe	Asp	Val	Glu	Leu	
				100					105				110			
cat	cat	tgc	aag	gtg	aat	att	tgg	cta	atg	agg	aag	caa	att	ttg	gct	385
His	His	Cys	Lys	Val	Asn	Ile	Trp	Leu	Met	Arg	Lys	Gln	Ile	Leu	Ala	
				115					120				125			
aat	aag	gaa	gaa	att	tct	aag	cag	caa	agc	att	caa	gag	gtg	act	tgg	433
Asn	Lys	Glu	Glu	Ile	Ser	Lys	Gln	Gln	Ser	Ile	Gln	Glu	Val	Thr	Trp	
				130					135				140			
gtg	ctg	tta	aag	gca	ttc	agt	ttc	ata	agg	gag	gca	gag	cat	aag	agt	481
Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg	Glu	Ala	Glu	His	Lys	Ser	
				145					150				155			160
tca	gaa	aat	ttg	cac	cct	gac	aat	gtg	ata	aaa	aag	aaa	aac	cca	ttt	529
Ser	Glu	Asn	Leu	His	Pro	Asp	Asn	Val	Ile	Lys	Lys	Lys	Asn	Pro	Phe	
				165					170				175			
tct	gag	ggg	aaa	ttc	aag	ctg	gct	gca	gaa	att	tgc	ata	tgt	aat	gag	577
Ser	Glu	Gly	Lys	Phe	Lys	Leu	Ala	Ala	Glu	Ile	Cys	Ile	Cys	Asn	Glu	
				180					185				190			
gag	ctg	aat	gtt	aat	cct	caa	gac	aat	ggg	gaa	aat	atc	tcc	tgg	aca	625
Glu	Leu	Asn	Val	Asn	Pro	Gln	Asp	Asn	Gly	Glu	Asn	Ile	Ser	Trp	Thr	
				195					200				205			
tgt	cag	agg	tct	tca	cag	cag	tcc	atc	aaa	tca	ctg	gcc	tgg	agg	cct	673
Cys	Gln	Arg	Ser	Ser	Gln	Gln	Ser	Ile	Lys	Ser	Leu	Ala	Trp	Arg	Pro	
				210					215				220			
agg	aga	aaa	tgg	ttt	tgt	ggg	aca	ggc	cca	ggg	tcc	ctg	tgc	tgt	gtg	721

Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val			
225	230	235	240
cag cct aga gac ttg gtg ccc tgt gtc cca gtt aat tca gct gtg gct			769
Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala			
245	250	255	
tca gag ggt gca agc ccc aag cct tgg cag ctt cca agt ggt gtt gag			817
Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu			
260	265	270	
cct gtg ggt gca aag aag tca aga att gag gtt tgg gaa cct cca atc			865
Pro Val Gly Ala Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile			
275	280	285	
aga ttt cag aag ata tat gga aac ccc tgg atg ccc agg cag aag ttt			913
Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe			
290	295	300	
gct gta ggg gtg ggg tcc tca tgg aga acc tct gca agg gta gta caa			961
Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln			
305	310	315	320
aag gga aat gtt ggg tgg gag ccc cca cac aga gtc ccc agt ggg gct			1009
Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala			
325	330	335	
cca tct agt aga gct gtg aga aga agt cca cca tcc tcc aga ctc cag			1057
Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln			
340	345	350	
aag ggt aga tcc act gac agc ttg cag cat gtg cct gaa aaa tcc aca			1105
Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr			
355	360	365	
gac act cag tgc cag cct gtg aaa gca gca ggg atg gag tct gta ccc			1153
Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro			
370	375	380	
tac aaa acc gta gtg gca gag ctg acc aag acc gtg gga atc tac ctc			1201
Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu			
385	390	395	400

ttg cat tgt cat gac ctg gac gtg aga cat gga gtc aaa aga gat cat 1249  
Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His  
405 410 415

ttt gga gct tta aga ttt gac tgc ccc act gga ttt cg<sup>g</sup> act tat atg 1297  
Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met  
420 425 430

ggg ccc gta ccc ctt tgt ttt ggc caa ttt ttt cca ttt gga act gcc 1345  
Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala  
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gta ttt acc caa tgc ctg tac ctc cat tgt atg tag / 1381  
Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met \* /  
450 455

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<212> PRT  
<213> *Homo sapiens*

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 20 25 30  
 Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met  
 35 40 45  
 Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys  
 50 55 60  
 Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly  
 65 70 75 80  
 Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe  
 85 90 95  
 Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu  
 100 105 110  
 His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala  
 115 120 125  
 Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp  
 130 135 140  
 Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser  
 145 150 155 160

Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe  
                  165                 170                 175  
 Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu  
                  180                 185                 190  
 Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr  
                  195                 200                 205  
 Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro  
                  210                 215                 220  
 Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val  
                  225                 230                 235                 240  
 Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala  
                  245                 250                 255  
 Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu  
                  260                 265                 270  
 Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile  
                  275                 280                 285  
 Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe  
                  290                 295                 300  
 Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln  
                  305                 310                 315                 320  
 Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala  
                  325                 330                 335  
 Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln  
                  340                 345                 350  
 Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr  
                  355                 360                 365  
 Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro  
                  370                 375                 380  
 Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu  
                  385                 390                 395                 400  
 Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His  
                  405                 410                 415  
 Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met  
                  420                 425                 430  
 Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala  
                  435                 440                 445  
 Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met  
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<211> 1377

<212> DNA

<213> Artificial Sequence

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<223> Degenerate polynucleotide encoding a polypeptide  
of SEQ ID NO:2

&lt;221&gt; variation

&lt;222&gt; (1)...(1377)

&lt;223&gt; Each n is independently A, T, G, or C.

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1377)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 3

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ccngcnccayc cnmgnccncc ngargargtn ggnccnccng gngcnccngg nytnccncar	120
tayacnggng arathwsnga ratgacnaar tgyccntgyc cngayathga rmgnwsngcn	180
ttyacngtna arytnwsngg naarytnccn ytnccnttya arccnathat httyacnggn	240
gtnynttaya aycncarmg ngayytnaar gargcnatgg gngtnnttygc ntgymngntn	300
ccnggnaayt aytaywsnws nttygaygtn garytncayc aytgyaargt naayathtgg	360
ytnatgmna arcarathyt ncnaayaar gargarathw snaarcara rwsnathcar	420
gargtnacnt gggtnytnyt naargcntty wsnttyathm gngargcnga rcayaarwsn	480
wsngaraayy tncayccnga yaaygttnath aaraaraara aycnttyws ngarggnaar	540
ttyaarytn gngcngarat htgyathtgty aaygargary tnaaygttnaa yccncargay	600
aayggngara ayathwsntg gacntgycar mgnwsnwsnc arcarwsnat haarwsnytn	660
gcntggmgnc cnmgmgnnaa rtggttytgy ggnacnggnc cnggnwsnyt ntgytgygtn	720
carccnmngng ayytngtncc ntgygttnccn gttnaaywsng cngtngcnws ngarggngcn	780
wsnccnaarc cntggcaryt nccnwsnggn gtngarccng tnngncnaa raarwsnmgn	840
athgargtgtt gggarccncc nathmgntty caraaratht ayggnaaycc ntggatgccc	900
mgnrcaraart tygcngtnng ntnggnwsn wsntggmgnna cnwsngcnmg ntngtnncar	960
aarggnaayg tnngntggta rccnccncay mgngtnccnw sngngcncc nwsnwsnmgn	1020
gcngtnmgnm gnwsnccncc nwsnwsnmgn ytncaaraarg gnmgrwsnac ngaywsnytn	1080
carcaygtnc cngaraarws nacngayacn cartgycarc cngtnaargc ngcnggnatg	1140
garwsngtnc cntayaarac ntngtnncn garytnacna aracngtnng nathtayytn	1200
ytncaytgyc aygayytna ygtngmncay ggnctnaarm gngaycaytt yggngcnytn	1260
mgnttygaty gycncacngg nttymgnacn tayatggnc cngtnccnyt ntgytgyggn	1320
carttattytc cnttyggnaac ngcngtnntty acncartgyy tntayytnca ytgyatg	1377

&lt;210&gt; 4

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<220>

<223> Aromatic motif

<221> VARIANT

<222> (2)...(6)

<223> Each Xaa is any amino acid residue

<221> VARIANT

<222> (7)...(7)

<223> Xaa is asparagine or aspartic acid

<221> VARIANT

<222> (8)...(11)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (12)...(12)

<223> Xaa is phenylalanine, tyrosine, tryptophan, or  
leucine

<221> VARIANT

<222> (13)...(18)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (20)...(24)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (26)...(26)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (28)...(31)

<223> Each Xaa is independently any amino acid residue

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Phe Xaa  
1 5 10 15  
Xaa Xaa Phe Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Xaa Xaa Xaa  
20 25 30

<210> 5  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(1731)

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Val Ile Glu His Val Glu Val Ala Gly Pro Pro Ala His Pro Arg Pro			
130	135	140	
cca gaa gaa gtg ggg cct cct ggt gca cca ggt tta cca caa tat aca			480
Pro Glu Glu Val Gly Pro Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr			
145	150	155	160
gga gaa ata agt gaa atg aca aaa tgc ccc tgt cct gat ata gaa agg			528
Gly Glu Ile Ser Glu Met Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg			
165	170	175	
tca gcc ttt act gtg aag ctc agt gga aaa ctt cct ctt cct ttc aag			576
Ser Ala Phe Thr Val Lys Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys			
180	185	190	.
ccc atc atc ttc aca ggg gtc ctg tac aat gcc cag agg gat tta aag			624
Pro Ile Ile Phe Thr Gly Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys			
195	200	205	
gag gcc atg gga gtc ttt gct tgc agg gtg cct ggg aat tac tac tcc			672
Glu Ala Met Gly Val Phe Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser			
210	215	220	
agc ttt gat gtt gag ctg cat cat tgc aag gtg aat att tgg cta atg			720
Ser Phe Asp Val Glu Leu His His Cys Lys Val Asn Ile Trp Leu Met			
225	230	235	240
agg aag caa att ttg gct aat aag gaa gaa att tct aag cag caa agc			768
Arg Lys Gln Ile Leu Ala Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser			
245	250	255	
att caa gag gtg act tgg gtg ctg tta aag gca ttc agt ttc ata agg			816
Ile Gln Glu Val Thr Trp Val Leu Leu Lys Ala Phe Ser Phe Ile Arg			
260	265	270	
gag gca gag cat aag agt tca gaa aat ttg cac cct gac aat gtg ata			864
Glu Ala Glu His Lys Ser Ser Glu Asn Leu His Pro Asp Asn Val Ile			
275	280	285	
aaa aag aaa aac cca ttt tct gag ggg aaa ttc aag ctg gct gca gaa			912
Lys Lys Lys Asn Pro Phe Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu			
290	295	300	

att tgc ata tgt aat gag gag ctg aat gtt aat cct caa gac aat ggg Ile Cys Ile Cys Asn Glu Glu Leu Asn Val Asn Pro Gln Asp Asn Gly 305               310               315               320	960
gaa aat atc tcc tgg aca tgt cag agg tct tca cag cag tcc atc aaa Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys 325               330               335	1008
tca ctg gcc tgg agg cct agg aga aaa tgg ttt tgt ggg aca ggc cca Ser Leu Ala Trp Arg Pro Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro 340               345               350	1056
ggg tcc ctg tgc tgt gtg cag cct aga gac ttg gtg ccc tgt gtc cca Gly Ser Leu Cys Cys Val Gln Pro Arg Asp Leu Val Pro Cys Val Pro 355               360               365	1104
gtt aat tca gct gtg gct tca gag ggt gca agc ccc aag cct tgg cag Val Asn Ser Ala Val Ala Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln 370               375               380	1152
ctt cca agt ggt gtt gag cct gtg ggt gca aag aag tca aga att gag Leu Pro Ser Gly Val Glu Pro Val Gly Ala Lys Lys Ser Arg Ile Glu 385               390               395               400	1200
gtt tgg gaa cct cca atc aga ttt cag aag ata tat gga aac ccc tgg Val Trp Glu Pro Pro Ile Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp 405               410               415	1248
atg ccc agg cag aag ttt gct gta ggg gtg ggg tcc tca tgg aga acc Met Pro Arg Gln Lys Phe Ala Val Gly Val Gly Ser Ser Trp Arg Thr 420               425               430	1296
tct gca agg gta gta caa aag gga aat gtt ggg tgg gag ccc cca cac Ser Ala Arg Val Val Gln Lys Gly Asn Val Gly Trp Glu Pro Pro His 435               440               445	1344
aga gtc ccc agt ggg gct cca tct agt aga gct gtg aga aga agt cca Arg Val Pro Ser Gly Ala Pro Ser Ser Arg Ala Val Arg Arg Ser Pro 450               455               460	1392
cca tcc tcc aga ctc cag aag ggt aga tcc act gac agc ttg cag cat	1440

Pro Ser Ser Arg Leu Gln Lys Gly Arg Ser Thr Asp Ser Leu Gln His			
465	470	475	480
gtg cct gaa aaa tcc aca gac act cag tgc cag cct gtg aaa gca gca			1488
Val Pro Glu Lys Ser Thr Asp Thr Gln Cys Gln Pro Val Lys Ala Ala			
485	490	495	
ggg atg gag tct gta ccc tac aaa acc gta gtg gca gag ctg acc aag			1536
Gly Met Glu Ser Val Pro Tyr Lys Thr Val Val Ala Glu Leu Thr Lys			
500	505	510	
acc gtg gga atc tac ctc ttg cat tgt cat gac ctg gac gtg aga cat			1584
Thr Val Gly Ile Tyr Leu Leu His Cys His Asp Leu Asp Val Arg His			
515	520	525	
gga gtc aaa aga gat cat ttt gga gct tta aga ttt gac tgc ccc act			1632
Gly Val Lys Arg Asp His Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr			
530	535	540	
gga ttt cg act tat atg ggg ccc gta ccc ctt tgt ttt ggc caa ttt			1680
Gly Phe Arg Thr Tyr Met Gly Pro Val Pro Leu Cys Phe Gly Gln Phe			
545	550	555	560
ttt cca ttt gga act gcc gta ttt acc caa tgc ctg tac ctc cat tgt			1728
Phe Pro Phe Gly Thr Ala Val Phe Thr Gln Cys Leu Tyr Leu His Cys			
565	570	575	
atg			1731
Met			

<210> 6  
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 <212> PRT  
 <213> Homo sapiens

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 Lys Cys Cys Ile Gly Glu Met Gly Tyr Met Arg Val Thr Met Gly Arg  
 20 25 30

Val Gly Ser Trp Arg Glu Leu Gly Lys Pro Ser Gly Ile Trp Glu Met  
           35                  40                  45  
 Ala Gly Asp Thr Glu Val Lys Lys Thr Gly Phe Leu Gln Glu Leu Thr  
       50                  55                  60  
 Phe Gln Gln Glu Pro Gly Ile Ser Ser Ser Pro Ser Cys Ser Arg Ser  
       65                  70                  75                  80  
 Cys His Val Thr Pro Pro Ala Pro Pro Ala Ser Ser Ala Ile Ile Val  
       85                  90                  95  
 Arg Phe Leu Arg Pro Ser Pro Glu Ala Asp Ala Ser Ser Met Leu Ile  
       100                  105                  110  
 Ala Gln Ser Val Glu Pro Ile Val Val Ile Pro Val Leu Ile Thr Ala  
       115                  120                  125  
 Val Ile Glu His Val Glu Val Ala Gly Pro Pro Ala His Pro Arg Pro  
       130                  135                  140  
 Pro Glu Glu Val Gly Pro Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr  
       145                  150                  155                  160  
 Gly Glu Ile Ser Glu Met Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg  
       165                  170                  175  
 Ser Ala Phe Thr Val Lys Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys  
       180                  185                  190  
 Pro Ile Ile Phe Thr Gly Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys  
       195                  200                  205  
 Glu Ala Met Gly Val Phe Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser  
       210                  215                  220  
 Ser Phe Asp Val Glu Leu His His Cys Lys Val Asn Ile Trp Leu Met  
       225                  230                  235                  240  
 Arg Lys Gln Ile Leu Ala Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser  
       245                  250                  255  
 Ile Gln Glu Val Thr Trp Val Leu Leu Lys Ala Phe Ser Phe Ile Arg  
       260                  265                  270  
 Glu Ala Glu His Lys Ser Ser Glu Asn Leu His Pro Asp Asn Val Ile  
       275                  280                  285  
 Lys Lys Lys Asn Pro Phe Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu  
       290                  295                  300  
 Ile Cys Ile Cys Asn Glu Glu Leu Asn Val Asn Pro Gln Asp Asn Gly  
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 Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys  
       325                  330                  335  
 Ser Leu Ala Trp Arg Pro Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro  
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 Gly Ser Leu Cys Cys Val Gln Pro Arg Asp Leu Val Pro Cys Val Pro  
       355                  360                  365

Val Asn Ser Ala Val Ala Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln  
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 Leu Pro Ser Gly Val Glu Pro Val Gly Ala Lys Lys Ser Arg Ile Glu  
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 Val Trp Glu Pro Pro Ile Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp  
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 Met Pro Arg Gln Lys Phe Ala Val Gly Val Gly Ser Ser Trp Arg Thr  
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 Ser Ala Arg Val Val Gln Lys Gly Asn Val Gly Trp Glu Pro Pro His  
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 Arg Val Pro Ser Gly Ala Pro Ser Ser Arg Ala Val Arg Arg Ser Pro  
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 Pro Ser Ser Arg Leu Gln Lys Gly Arg Ser Thr Asp Ser Leu Gln His  
     465                  470                  475                  480  
 Val Pro Glu Lys Ser Thr Asp Thr Gln Cys Gln Pro Val Lys Ala Ala  
     485                  490                  495  
 Gly Met Glu Ser Val Pro Tyr Lys Thr Val Val Ala Glu Leu Thr Lys  
     500                  505                  510  
 Thr Val Gly Ile Tyr Leu Leu His Cys His Asp Leu Asp Val Arg His  
     515                  520                  525  
 Gly Val Lys Arg Asp His Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr  
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 Gly Phe Arg Thr Tyr Met Gly Pro Val Pro Leu Cys Phe Gly Gln Phe  
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 Met

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<211> 1731

<212> DNA

<213> Artificial Sequence

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of SEQ ID N0:6

<221> misc\_feature

<222> (1)...(1731)

<223> n = A,T,C or G

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cargarytna cnttycarca rgarcngn athwsnwsnw snccnwsntg ywsnmgnwsn	240
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